Table 1

S. aureus - Coding regions containing known sequences

1 2 2773 2422 mah/X2243183AB Saurenes agath, aggra and hid genes and for part of easy genes 10 10 10 10 10 10 10 1	Contig ORF	IORF	Start (nt)	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt length
1 867 2422 seeb MASS2431 Stand Stauteness agents, large	-		1419	1 757	emb X17301 SAHD	DNA for hld gene and for part of agr	100	663	663
1 867 439 6410 13572 6420 147710 15772 1572700 15840 1572700 15840 1		1 2	3273	1 2452	emb X52543 SAAG	agrA, agrB and hld	1 66	608	822
1 867 439 semb X72700 SMV S. aureus genes for S and P components of Panton-Valentine Hencocidins 95 1 66 904 901 122288 Stabblylococcus aureus gyrase-like protein alpha and beta subbunit (grib, and grib) 95 2 5302 6246 9091 33773 Stabblylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, graphylococcus aureus bkh sequence encoding three ORFs, complete cds, graphylococcus aureus bkh sequence encoding three ORFs, complete cds, graphylococcus aureus bkh sequence encoding three ORFs, complete cds, graphylococcus aureus bkh sequence encoding three ORFs, complete cds, graphylococcus aureus bkh sequence encoding three ORFs, complete cds, graphylococcus aureus bkh sequence encoding three ORFs, complete cds, graphylococcus aureus pptiloglycan hydrolase gene, complete cds, graphylococcus aureus genes gland gene encoding lipase (glycerol extern phydrolase) gene,		5	6418	1 5651	j D14711 STAH	aureus HSP10 and HSP60	86	223	768
4 5031 3571 emb 772700 SAPV Staureus genes for S and P components of Panton-Valentine Leucocidins 95 8 86 904 490 1252288 Staphylococcus aureus gyrass-like protein alpha and beta subunit (gill and grant 1918) 1918 191			1 807	439		aureus genes for S and F components of	81	216	369
1 866 9044 901 19152288 Staphylococcus aureus gyrase-like protein alpha and beta subunit (971h and 1918) 1918 1918 19183773 Staphylococcus aureus prolipoprotein diacylglyceryl transferase (1917) gene, 94 19183773 Staphylococcus aureus prolipoprotein diacylglyceryl transferase (1917) gene, 95 1918 19183773 Staphylococcus aureus prolipoprotein diacylglyceryl transferase (1917) gene, 95 1918 19183773 Staphylococcus aureus prolipoprotein diacylglyceryl transferase (1917) gene, 95 1918 19183773 Staphylococcus aureus pholipoprotein diacylglyceryl transferase (1917) gene, 95 1918 19183773 Staphylococcus aureus pholipoprotein diacylglyceryl transferase (1917) gene, 95 1918 19183773 Staphylococcus aureus pholipoprotein diacylglyceryl transferase (1917) gene, 95 1918 19183773 Staphylococcus aureus pholipoprotein diacylglyceryl transferase (1917) gene, 95 1918 19183773 Staphylococcus aureus pholipology, 5 flank 1918 19183773 Staphylococcus aureus pholipology, 5 flank 1918 19183774 Staphylococcus aureus popticology, 5 flank 1918 1918374 Staphylococcus aureus popticology, 5 flank 1918 1918374 Staphylococcus aureus popticology, 5 flank 1918 19	5	4 -	5031	3571	emb X72700 SAPV	genes for S and F components of Panton-Valentine	95	424	1461
5 5302 6246 90 U35773 Istaphylococcus aureus prolipoprotein diacylglyceryl transferase [1gt] gene, 99 190 U35773 Istaphylococcus aureus prolipoprotein diacylglyceryl transferase [1gt] gene, 99 190	10		986	904		aureus gyrase-like protein alpha and beta subunit (grlA complete cds	86	. 715	819
6 6249 7091 gplU35773 Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, 99 1784 gplU35773 Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, 99 1784 gplU3930 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 1784 gplL19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 1786 gplL19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 1786 gplL19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 1786 gplL19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 1786 gplL19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 1786 gplL19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 1786 gplL19300 Staphylococcus aureus peptidodlycan hydrolase gene, complete cds, 100 1786	16		1 5302	6246		aureus prolipoprotein diacylglyceryl transferase (lgt)	40	251	945
1 1995 549 qpli1937731 Staphylococcus aureus DRA sequence encoding three ORFs, complete cds 100 1 995 549 qpli193001 Staphylococcus aureus DRA sequence encoding three ORFs, complete cds 100 2 1011 841 qpli193001 Staphylococcus aureus DRA sequence encoding three ORFs, complete cds 100 3 2010 1738 qpli193001 Staphylococcus aureus DRA sequence encoding three ORFs, complete cds 100 4 5300 3825 qplM767141 Staphylococcus aureus ppptidoglycan hydrolase gene, complete cds 100 5 4788 4282 qplM767141 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 6 4788 4282 qplM767141 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 7 145 145 qplM10721 Staphylococcus aureus isoleucyl-tRNA synthetase (iles) gene, partial cds 99 8 155 qplM10721 Staphylococcus aureus isoleucyl-tRNA synthetase (iles) gene, partial cds 99 9 140 14077 11463 emb X73889 SAP1 S.aureus genes Pl and PZ 140 140 14 14977 11463 emb X73889 SAP1 S.aureus genes Pl and PZ 14284 13112 qplM127151 S.aureus genes Pl and PZ 14284 13112 qplM127151 S.aureus genes Pl and PZ 14284 13112 qplM127151 S.aureus gene Got	16	۰ – –	6249	1 7091		aureus prolipoprotein diacylglyceryl transferase (lgt)	66	843	843
1 995 549 gb LL9300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; 100 2 1011 841 gb LL9300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; 91 3 2010 1798 gb LL9300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; 100 4 5330 3325 gb M/6714 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 5 4788 4282 gb M/6714 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 1 2 145 gb U41072 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 2 84 557 gb U41072 Staphylococcus aureus isoleucyl-RNA synthetase (11e5) gene, partial cds 99 3 763 3531 emb X7421918A11 Staureus gene for isoleucyl-RNA synthetase (11e5) gene, partial cds 99 4 14977 113453 emb X7421918A1 Staureus genes Pl and P2 91 5 1424 11355 emb X7388919AP1 Staureus genes Pl and P2 91 6 14977 113454 12518 qb M12715 Staureus gene encoding lipase (qlycerol ester hydrolase) 100 7 11424 11518 qb M12715 Staureus gene encoding lipase (qlycerol ester hydrolase) 100 8 11 11424 11518 qb M12715 Staureus gene encoding lipase (qlycerol ester hydrolase) 100 9 110 110 110 110 110 110 11148 11518 qb M12715 Staureus gene encoding lipase (qlycerol ester hydrolase) 100 10 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110	16	7	7084	1 7584		aureus prolipoprotein diacylglyceryl transferase (lgt)	66	342	501
2 1011 841 9b L19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; 91 1 1 2 1 1798 9b L19300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; 100 1 1 1 1 1 1 1 1	50		1 995	549		aureus DNA sequence encoding three ORFs, complete 11 sequence homology, 5' flank	100	443	447
3 2010 1798 gb LL9300 Staphylococcus aureus DNA sequence encoding three ORFs, complete cds, 100 4 5300 3825 gb M76714 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 5 4788 4282 gb M76714 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 1 2 145 gb U41072 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 2 84 557 gb U41072 Staphylococcus aureus isoleucyl-tRNA synthetase (iles) gene, partial cds 99 3 763 3531 emb X74219 SAII S.aureus gene for isoleucyl-tRNA synthetase (iles) gene, partial cds 99 4 14977 13465 emb X73889 SAP1 S.aureus genes Pl and P2 99 5 14241 13855 emb X73889 SAP1 S.aureus genes Pl and P2 99 6 17 14284 13112 gb M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 7 14344 15518 gb M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 8 130 130 130 130 130 130 130 9 131	50		1011	841		aureus DNA sequence encoding three ORFs, complete 11 sequence homology, 5' flank	91	137	171
4 5300 3825 gph M76714 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 5 4788 4282 gph M76714 Staphylococcus aureus isolaucyl-tRNA synthetase (ileS) gene, partial cds 100 1 2 145 gbh U41072 Staphylococcus aureus isolaucyl-tRNA synthetase (ileS) gene, partial cds 99 3 763 3531 emb X74219 SAIL S.aureus gene for isolaucyl-tRNA synthetase (ileS) gene, partial cds 99 3 1261 4392 gbh U66665 Staphylococcus aureus DNA fragment with class II promoter activity 100 4 14977 113463 emb X73889 SAP1 S.aureus genes P1 and P2 99 5 14241 113855 emb X73889 SAP1 S.aureus genes P1 and P2 91 6 17 14284 113112 gph M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 7 14343 15518 gph M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 8 100	50	m 	2010	1798		aureus DNA sequence encoding three ORFs, 11 sequence homology, 5' flank	100	110	213
5 4788 4282 gb M76714 Staphylococcus aureus peptidoglycan hydrolase gene, complete cds 100 1 2 145 gb U41072 Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds 100 2 84 557 gb U41072 Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds 99 3 763 3531 emb X74219 SAIL S.aureus gene for isoleucyl-tRNA synthetase (ileS) gene, partial cds 99 4 14977 13463 emb X73889 SAP1 S.aureus genes Pl and P2 100 5 14241 113855 emb X73889 SAP1 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 6 113434 15518 gb M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 7 14284 15518 gb M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 8 100 9	1 20	4	1 5300	1 3825	gb M76714	aureus peptidoglycan hydrolase gene, complete	100	948	1476
1 2 145 gb U41072 Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds 100 2 84 557 gb U41072 Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds 99 3 763 3531 emb X74219 SAIL S.aureus gene for isoleucyl-tRNA synthetase 110 100 3 1261 4392 gb U66665 Staphylococcus aureus DNA fragment with class II promoter activity 100 14 14977 13463 emb X73889 SAP1 S.aureus genes P1 and P2 99 15 14241 13152 gb MX73889 SAP1 S.aureus gene encoding libase (glycerol ester hydrolase) 100 17 14284 13112 gb MX2715 S.aureus gene encoding libase (glycerol ester hydrolase) 100 19 13434 15518 gb MX2715 S.aureus gene encoding libase (glycerol ester hydrolase) 100	1 20	5	1 4788	1 4282		aureus peptidoglycan hydrolase gene, complete	100	309	507
2 84 557 gb U41072 Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds 99 13 763 3531 emb X74219 SAIL S.aureus gene for isoleucyl-tRNA synthetase 1 99 1 1 1 1 1 1 1	1 26		7	145		aureus isoleucyl-tRNA synthetase (ileS) gene, partial	100	126	144
3 763 3531 emb X74219 SAIL S.aureus gene for isoleucyl-tRNA synthetase 3 1261 4392 gb U66665 Staphylococcus aureus DNA fragment with class II promoter activity 100 14 14977 13463 emb X73889 SAP1 S.aureus genes Pl and P2 99 15 14241 13185 emb X73889 SAP1 S.aureus genes Pl and P2 99 17 14284 13112 gb M12715 S.aureus gene encoding libase (glycerol ester hydrolase) 100 19 13434 15518 gb M12715 S.aureus gene encoding libase (glycerol ester hydrolase) 100	26	- 5	84	1 557		aureus isoleucyl-tRNA synthetase (ileS) gene, partial	66	430	474
3 1261 4392 gb U66665 Staphylococcus aureus DNA fragment with class II promoter activity 100 14 14977 13463 emb X73889 SAPI S.aureus genes Pl and P2 99 15 14241 13855 emb X73889 SAPI S.aureus genes Pl and P2 98 17 14284 13112 gb M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100 19 13434 15518 gb M12715 S.aureus gene encoding lipase (glycerol ester hydrolase) 100	1 26	3	1 763	1 3531	emb X74219 SAIL	gene for isoleucyl-tRNA	1 66	2769	2769
14 14977 13463 emb X73889 SAPI S.aureus genes Pl and P2 15 14241 13855 emb X73889 SAPI S.aureus genes Pl and P2 17 14284 13112 gb M12715 S.aureus geh gene encoding lipase (glycerol ester hydrolase) 100 19 13434 15518 gb M12715 S.aureus geh gene encoding lipase (glycerol ester hydrolase) 100 10	1 29	- 3	1261	4392		aureus DNA fragment with class II promoter	100	117	3132
15 14241 13855 emb X73889 SAP1 S.aureus genes P1 and P2	31	114	114977	113463	emb X73889 SAP1	genes P1 and	66	1351	1515
17 14284 13112 gb M12715 S.aureus geh gene encoding lipase (glycerol ester hydrolase) 100	31		114241	13855	emb X73889 SAP1	genes P1 and	1 86	258	387
	38	117	114284	113112		geh gene encoding lipase (glycerol	100	372	1173
	38	119	13434	115518		geh gene encoding lipase (glycerol	100	2085	2085

Table 1

S. aureus - Coding regions containing known sequences

46 2 23.9 11727 (2017)33341 Stabbbliococcus anneas type is captule quase, captul,	Contig ORF	-+ IORF	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
1720 2239 499 49737314 Stephylococcus automatory pages capable genes, cap88, cap8	46	2	519	1727		aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8C, cap8C, cap8H, cap8I, cap8I, cap8K, cap8K, cap8M, complete cds	866	1209	1209
4 2259 3182 (ph 073374 Staphy) dococcus aureus type 8 capalle genes, cap88, cap88	4 46	 m 	1720	1 2295	gb U73374 	aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8G, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, ccmplete cds	86	576	576
1 1 1 1 1 2 1935 1917 Staphylococcus aureus type 6 capeule genes, cap88, ca	46	+ ·	2259	3182		aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8G, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, complete cds	97	924	924
6 4336 5720 401U73374 Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8G, cap	46		3173	4498		aureus type 8 capeule genes, cap8A, cap8B, cap8C, cap8C, cap8C, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, complete cds	866	1283	1326
1 2 955 6120 491/13374 Staphylococcus aureus type 8 capsule genes, cap84,	96	9	4536	5720	gb U73374 	aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8C, cap8C, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, complete cds	86	1185	1185
1 2 955 gbl.L258931 Staphylococcus aureus reck gene, complete cds 99 100 1	9		6455	6120	gb U73374 	aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8G, cap8C, cap8H, cap8I, cap8U, cap8K, cap8L, cap8M, complete cds	66	278	336
3 4465 2924 embl X850291 SAAH S. aureus AhpC gene 3 5074 3392 embl X820292 ISAFN S. aureus finbB gene for fibronectin binding protein B 99 100 1 1 1 1 1 1 1 1	48		2	955	gb L25893	aureus recA gene,	66	954	954
4 4108 3315 emb X85029 SAFN S. aureus fnbB gene for fibronectin binding protein B 100 1 1 1 1 1 1 1 1	1 50	8	1 4465	1 2924	i 1		100	88	1542
3 5074 3392 emb X62992 SAFN S.aureus fnbB gene for fibronectin binding protein B 100 1 1 1 1 1 1 1 1	1 50	4	1 4108	3515	emb X85029 SAAH	Ahpc	86	540	594
4 4865 4122 emb X62992 SAFN S. aureus fnbB gene for fibronectin binding protein B 99 100 1 100 1 100 1 1 1	54	. 3	1 5074	3392		fnbB gene for fibronectin binding protein	100	1668	1683
5 5056 4562 emb X62992 SAFN S.aureus fibronectin-binding protein (fnbA) mkNA, complete cds 100 3 1743 2819 emb X87104 SADN S.aureus fibronectin-binding protein (fnbA) mkNA, complete cds 100 3 1743 2819 emb X97786 SAPB S.aureus abcA, pbp4, and tagD genes 1743 1743 1744 1745	1 54	4	1 4865	4122	emb X62992 SAFN	fnbB gene for fibronectin binding protein	1 66 1	720	744
6 11386 8300 gbl/J04151 S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds 100 3 3 174 2858 3280 embix91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 4 2858 3280 embix91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 1 1 1 1 1 1 1	1 54	2	1 5056	1 4562		fnbB gene for fibronectin binding protein	100	463	495
3 1743 2819 emb X89104 SADN S.aureus abcA, pbp4, and tagD genes 4 2858 3280 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 5 6005 4701 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 6 5677 5378 gb U029478 Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, 100 7 5086 6840 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 888 445 gb M21854 S.aureus agr gene encoding an accessory gene regulator protein, complete 100 888 445 gb M21854 S.aureus agrA, agrB and hld genes 99 1	1 54	9	111386	1 8300	gb J04151	fibronectin-binding protein (fnbA) mRNA, complete	100	3087	3087
4 2858 3280 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 5 6005 4701 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 6 5677 5378 gb U29478 Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, 100 1 5086 6840 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 1 1 888 445 gb M21854 S.aureus agr gene encoding an accessory gene regulator protein, complete 100 1 1 1 1 1 1 1 1	28		11743	1 2819		mdr, pbp4 and taqD	89	89	1077
5 6005 4701 emb[X91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 6 5677 5378 gblU29478 Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, 100 1 5086 6840 emb[X91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 1 888 445 gblM21854 S.aureus agr gene encoding an accessory gene regulator protein, complete 100	28	4	1 2858	3280		abcA, pbp4,	66	423	423
6 5677 5378 gb U29478 Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, 100 7 5086 6840 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 7 888 445 gb M21854 S.aureus agr gene encoding an accessory gene regulator protein, complete 100 1 888 445 gb M21854 S.aureus agr gene accessory gene regulator protein, complete 100 2 2457 1453 emb X52543 SAAG S.aureus agrA, agrB and hld genes	28	- 2	1 6005	4701	emb x91786 SAPB	abcA, pbp4, and tagD	1 66 1	1305	1305
7 5086 6840 emb X91786 SAPB S.aureus abcA, pbp4, and tagD genes 99 1 888 445 gb M21854 S.aureus agr gene encoding an accessory gene regulator protein, complete 100	58	9	1 5677	5378		aureus ABC transporter-like protein AbcA (abcA)	100	300	300
1 888 445 gb M21854 S.aureus agr gene encoding an accessory gene regulator protein, complete 100	28	7	9805	1 6840	emb X91786 SAPB	pbp4,	1 66 1	1755	1755
2 2457 1453 emb XS22543 SAAG S.aureus agrA, agrB and hld genes	72		888	1 445	gb M21854 	agr gene encoding an accessory gene regulator protein,	100	444	444
	72	5	1 2457	1453	emb X52543 SAAG	agrB and hld	1 66 1	673	1005

Table 1

S. aureus - Coding regions containing known sequences

Contig	ORF	Start (nt)	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt
82		357	3917	emb X64172 SARP 	IS.aureus rplL, orf202, rpcB(rif) and rpcC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	66	2396	3561
82	- 5	4027	7677	emb X89233 SARP	S.aureus DNA for rpoC gene	66	3171	3651
82		7745	8008	gb U20869	IStaphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, $ $ ribosomal protein S7 (rpsG) and ORF I genes, partial cds	100	320	324
82	4	8103	8579	gb U20869 	istaphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, $ $ ribosomal protein S7 (rpsG) and ORF I genes, partial cds	100	477	477
82	ν - – –	8618	8821	gb U20869	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF I genes, partial cds	1000	154	204
84		18	191	lgb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8H, cap8I, cap8V, cap8K,	866	164	174
84	2	189	893	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8E, cap8E, cap8E, cap8W, cap8N, cap8O, cap8P, complete cds	94	705	705
8	E	887	1660	1gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8H, cap8I, cap8A, cap8K, cap8E, cap8F, cap8N, cap8O, cap8P, complete cds	66	774	774
84	4	1584	3503	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8F, cap8W, cap8N, cap8V, cap8F, complete cds	86	1920	1920
84	2	3394	4521	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8E, cap8E, cap8H, cap8I, cap8U, cap8K, cap8E, cap8E, complete cds	97	1128	1128
84	9	4519	5643	gb U73374 	Staphylococcus aureus type θ capsule genes, capθλ, capθΒ, capθC, capθD, capθE, capθF, capθF, capθH, capθJ, capθK, capθE, capθH, capθJ, capθH, capθO, capθH, capθO, capθO	97	1125	1125
96	1 2	1245	1 3896	emb 218852 SACF	S.aureus gene for clumping factor	83	099	2652
97	2	625	1 882	gb U41072	Staphylococcus aureus isoleucyl-tRNA synthetase (iles) gene, partial cds	1 26	89	258
111	7	m 	452	gb L41499	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	100	450	450
111	2	526	1041	gb L41499 	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	66	516	516
117	2	1278	1958	gb M83994	Staphylococcus aureus prolipoprotein signal peptidase (1sp) gene, complete cds	100	61	681

Table 1

S. aureus - Coding regions containing known sequences

Contig 10	ORF St ID (n	Start (nt)	Stop	match	match gene name	percent ident	HSP nt length	ORF nt length
ļ ·	4 37	3787	4254	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	66	467	468
	4 25	2597	3640	emb X13290 SATN	Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon Tn4003	78	956	1044
:	5 1 38	3813 +	4265	emb 216422 SADI	S.aureus dfrB gene for dihydrofolate reductase	86	416	453
	6 43	4309	5172	emb 216422 SADI	S.aureus dfrB gene for dihydrofolate reductase	- 86	607	864
 	4 5296	 	6207	emb X71437 SAGY	S.aureus genes gyrB, gyrA and recF (partial)	1 76	838	912
 	5 11680		8987	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	2694	2694
 -	6 12886	į	110940	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	66	1947	1947
	7 12592	!	111765	dp 877055	recF cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	1 66	822	828
<u>.</u> – ·	3 1 41	4171	2867	167636U1dp1	Staphylococcus aureus S-adenosylmethionine synthetase gene, complete cds	66	1305	1305
	4 - 31	3100	4281	gb L42943	Staphylococcus aureus (clone KIN50) phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	100	1170	1182
	5 42	4254	4718	gb U51133	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	100	449	465
	69 - 6	1 7769	7261	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o- succinylbenzoic acid synthetase (menc) genes, complete cds	100	75	285
=-	110 1 94	9464	8361	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o- succinylbenzoic acid synthetase (menc) genes, complete cds	100	1104	1104
=	11 11232	 	97,48	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o- succinylbenzoic acid synthetase (menc) genes, complete cds	100	1485	1485
= - :	112 10739	!	110320	gb U51132	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o- succinylbenzoic acid synthetase (menc) genes, complete cds	100	332	420
	5 24	2454	3437	emb X58434 SAPD	IS.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	66	305	984
	6 1 35	3513	4820	emb X58434 SAPD	18.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	86	1308	1308
 	7 48	4818	6230	emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	66	1413	1413
	1 387		1526	gb 877055	recF cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	66	1140	1140
 	2 - 18	1877	2152	gb S77055	recF cluster: dnaA-replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	100	276	276
+	+							

Table 1

S. aureus - Coding regions containing known sequences

Contig		Start (nt)	Stop	match acession	match gene name	percent jercent ident	HSP nt length	ORF nt
153	m 	2143	1 2289	gb s770551	recF cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	66	113	147
154	110	110792	9314	gb U064511	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	91	154	1479
154	111	9935	9615	gb U064511	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	1 66	229	321
154	112	9943	110167	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	94	123	225
154	113	110089	111501	gb U064511	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	- 66	1326	1413
159	1 2	2195	1212	dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100 +	7.1	984
161	m 	2596	2270	gb M83994	Staphylococcus aureus prolipoprotein signal peptidase (1sp) gene, complete cds	92	203	327
162		1406	1 705	gb U21221	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	100	702	702
163		1263	1 1772	gb U19770	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	127	510
1 164	7	1 4774	1 9117	dbj D86727 D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	66	3470	4344
168		7448	6447	gb U21636 	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	100	1002	1002
168	œ 	9538	1 7961	gb U21636 	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	66	1158	1578
173	9	9240	1 7801	gb J03479; 	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	100	1440	1440
173		111252	9522	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	66	1731	1731
1 173	· -	8285	8704	gb J03479 	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	100	420	420
173	o	10168	9839	gb J03479 	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	100	330	330
173	110	111815	110829	emb X14827 SALA	Staphylococcus aureus lacC and lacD genes	100	786	987
173	111	112721	111774	emb X14827 SALA	Staphylococcus aureus lacC and lacD genes	100	948	948
1 173	112	112838	112305	gb M64724	S.aureus tagatose 6-phosphate isomerase gene, complete cds	100	534	534
173	-113	13243	112773	gb M32103 	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	471	471
173	14	114633	113866	gb M32103	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	768	168
1								

Table

S. aureus - Coding regions containing known sequences

-						+	+	+
Contig ORF	ORF	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
178		2	655	gb U52961	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	115	654
178	7	1 2201	1482	gb U52961	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	720	720
1 178	e 	1 2361	1909	gb U52961	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	453	453
178		1551	1853	gb U52961 	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	303	303
1 178	- 5	3541	12777	gb L42945	Staphylococcus aureus lytS and lytR genes, complete cds	66	765	765
1 178	9 -	3294	3025	gb L42945	Staphylococcus aureus lytS and lytR genes, complete cds	1 66	270	270
1 181		1114	1 590	gb M63171	S.aureus sigma factor (plaC) gene, complete cds	1 66	499	525
182		. 3	341	emb x61307 SASP	Staphylococcus aureus spa gene for protein A	1 86	277	339
1 182	1 2	069	1 2312	gb J01786	S.aureus spa gene coding for protein A, complete csd	97	1332	1623
1 182	<u>ا</u> س	1 5861	4251	emb x61307 sASP	Staphylococcus aureus spa gene for protein A	1 66	119	1611
185	 	m 	824	gb U31979	Staphylococcus aureus chorismate synthase (aroc) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	06	132	822
191	8 -	841	1 2760	lemb X17679 SACO	Staphylococcus aureus coa gene for coagulase	1 66	1920	1920
1 191	4 -	1 2967	3143	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	66	177	177
191	ر ا ا	5768	1 4566	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	66	250	1203
196	 	1741	872	gb L36472	Staphylococcus aureus lysyl-ERNA sythetase gene, complete cds, transfer RNA (tRNA) genes, 5S ribosomal RNA (5S rRNA) gene, 16S ribosomal RNA (16S RNNA) gene, 23S ribosomal RNA (23S rRNA) gene	66	870	870
1 198		1688	1 2011	emb x93205 SAPT	S.aureus ptsH and ptsI genes	66	324	324
1 198	4	1 2005	1 2310	emb x93205 SAPT	S.aureus ptsH and ptsI genes	97	304	306
1 202		163	1 1305	emb X97985 SA12	S.aureus orfs 1,2,3 & 4	66	1143	1143
1 202	- 2	1303	2175	emb X73889 SAP1	S.aureus genes P1 and P2	94	444	873
1 210		3114	1558	dbj D17366 STAA		1 66	1552	1557
210	. – –	1 2939	1 2232	gb L41499	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	1 66	684	708
214	=	1 7429	1770	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	96	157	342
1			1 1 1 1 1 1 1	*****				-

Table 1

| ORF nt | length | percent| HSP nt ident | length |dbj||D30690|STAN |Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete |dbj|D30690|STAN |Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete |dbj||D30690|STAN |Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete |dbj||D30690|STAN |Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete |dbj|D30690|STAN |Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete dbj|D30690|STAN |Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete |dbj|D21131|STAS|Staphylococcus aureus gene for a participant in homogeneous expression of | high-level methicillin resistance, complete cds |Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) |Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete |Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds (Staphylococcus aureus glycerol ester hydrolase (lip) gene, complete cds IStaphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, l cap8E, cap8E, cap8E, cap8H, cap8H, cap8H, cap8H, cap8H, cap8H, |emb|X72700|SAPV |S.aureus genes for S and F components of Panton-Valentine leucocidins emb|X62288|SAPE |S.aureus DNA for penicillin-binding protein 2 Staphylococcus aureus scdA gene, complete cds (Staphylococcus aureus sarA gene, complete cds Staphylococcus aureus scdA gene, complete cds cap80, cap8P, complete cds |emb|X97985|SA12 |S.aureus orfs 1,2,3 & 4 gene, complete cds | match gene name acession |gb|L19298| 1gb1U488261 1gb|U46541| 1gb | U57060 | |gb|M90693| |gb|U73374| |gb|125426| 1gb | U57060 | 1 2485 110816 | 110034 1 2728 1 2035 1 5176 1 3148 1 1093 Contig | ORF | Start | Stop ID | ID | (nt) | (nt) 1 5883 1 6334 1 5322 1 2979 | 5 | 7044 1 1 2855 3 | 2648 1 4 | 3120 1 3826 1 3 | 1973 1 4359 2 | 1694 11 12 1 2 | 388 1 1 2 œ ლ — <u>~</u> _ ~

S. aureus - Coding regions containing known sequences

 Table 1

S. aureus - Coding regions containing known sequences

Contig	IORF	+ Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt
265	5	889	476	dbj D21131 STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	+ 66 	213	213
1 265		2418	1765	dbj D21131 STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	86	69	654
1 266		1 2	1018	dbj D14711 STAH	Staphylococcus aureus HSP10 and HSP60 genes	86	743	1017
1 282			1 525	gb S72488	hemB=porphobilinogen synthase [Staphylococcus aureus, SA1959, Genomic, 1087 nt]	100	110	525
1 282	2	1 516	1502	gb S72488	hemB=porphobilinogen synthase [Staphylococcus aureus, SA1959, Genomic, 1087 nt]	1000	952	987
284		m 	170	gb M63176 	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	86	84	168
284	7	1 282	1034	gb M63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	712	753
284		1028	1 2026	gb M63176 	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	66	979	666
1 284	4	1990	1 2202	gb M63176 	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	86	187	213
289	e 	1536	1991	gb M32470	S.aureus Sau3AI-restriction-enzyme and Sau3AI-modification-enzyme genes,	66	338	456
303		7	898	gb L01055 	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	66	867	867
303	7	1409	1 2383	gb L01055	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hgLC) genes, complete cds	100	975	975
303	m 	1 2367	3161	gb L01055 	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	66	793	795
305		1 2707	1355	dbj D17366 STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	66	1343	1353
311		1 2628	1315	gb L42945	Staphylococcus aureus lytS and lytR genes, complete cds	86	1314	1314
312	9	7019	1 7870	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	74	351	852
323		1998	1003	gb U31175	Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase (ddh) gene, complete cds	86	966	1 966
326		1	1 237	lemb Y00356 SASP	Staphylococcus aureus V8 serine protease gene	100	108	237
338		1 687	388	emb X64389 SALE	S.aureus leuf-P83 gene for F component of leucocidin R	86	259	300
338	- 5	1 1828	1088	emb X64389 SALE	S.aureus leuF-P83 gene for F component of leucocidin R	97	137	741
			-					_

Table

| ORF nt | length 1146 657 540 216 1248 324 708 807 168 657 732 228 501 537 672 903 405 507 762 216 432 1176 1146 349 1248 200 151 percent| HSP nt ident | length 732 172 537 671 747 89 389 178 163 216 188 432 134 657 187 97 100 86 96 66 75 86 16 66 66 66 66 100 100 66 96 100 100 100 100 97 100 |Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, Staphylococcus aureus prolipoprotein signal peptidase (1sp) gene, complete Staphylococcus aureus prolipoprotein signal peptidase (1sp) gene, complete |dbj|D28879|STAP |Staphylococcus aureus gene for penicillin-binding protein 1, complete cds |dbj|D17366|STAA |Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs |dbj|D28879|STAP |Staphylococcus aureus gene for penicillin-binding protein 1, complete cds |dbj||D86240||D862 |Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, |emb|X17688|SAFE |S.aureus factor essential for expression of methicillin resistance (femA)
| |dbj||D86240||D862 |Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, (plc) staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) (plc) (plc) sures phosphatidylinositol-specific phospholipase C (plc) lasp23=alkaline shock protein 23 (methicillin resistant) [Staphylococcus aureus, 912, Genomic, 1360 nt] |Transposon In5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus MHC class II analog gene, complete cds |Staphylococcus aureus SA4 FtsZ (ftsZ) gene, complete cds (S.aureus (strain RN450) transposon In554 insertion site (S.aureus bacteriophage phi-11 attachment site (attB) |emb|X13404|SAHL |Staphylococcus aureus hlb gene for beta-hemolysin |emb|X62288|SAPE |S.aureus DNA for penicillin-binding protein 2 |emb|x62282|SATS |S.aureus target site DNA for IS431 insertion |emb|X61716|SAHL |S.aureus hlb gene encoding sphingomyelinase | dltC and dltD genes, complete cds | dltC and dltD genes, complete cds | Staphylococcus aureus) DNA |emb|V01281|SANU |S.aureus mRNA for nuclease gene, complete cds I gene, complete cds | match gene name | complete cds cds cds acession gb | M20393 | |gb|L19298| |gb|S76213| |gb|L41499| |gb|L43098| |gb|U06462| |gb|M83994| gb | L19298 | 1gb | K02985 | match | gb | M83994 | gb | U20503 | 2509 1 1148 1754 1 1046 1248 11187 1049 1 1507 Contig |ORF | Start | Stop ID |ID | (nt) | (nt) 1248 540 639 1 325 434 11122 666 | 1 685 217 516 1 903 808 1 230 1 674 1693 1810 1262 1829 1904 1 1 1 1341 1016 1582 2 | 1103 12 | 579 854 832 1 517 რ _ 1 1 865 1 1 1 457 - -5 m 7 ~ -----7 _ - 2 7 -<u>ო</u> 7 7 7 N 373 342 344 349 353 353 361 389 400 400 408 418 418 421 422 427 435 435 1 436 361 427

S. aureus - Coding regions containing known sequences

Table 1

S. aureus - Coding regions containing known sequences

Contig	ORF	Start (nt)	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt length
436	7	1 2403	1657	emb X17688 SAFE	IS.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	100	294	747
1 442	-	347	1300	emb X72700 SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	84	204	954
445	2	1 1906	2178	gb L01055	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	86	187	273
1 447	 	167	1078	19770101dg1	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	100	51	912
447	7	11176	1784	10776IU dg	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	597	609
1 454		1 7309	4319	emb 218852 SACF	S.aureus gene for clumping factor	75	653	2991
472	4	1 7896	1 5479	gb 125288 	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	66	2418	2418
472	 -	8120	6792	gb L25288	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	66	1328	1329
475	- 5	1 566	688	emb X52543 SAAG	S.aureus agrA, agrB and hld genes	100	76	324 1
481	<u></u>	1 1922	1560	emb X64172 SARP 	IS.aureus rpll, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta s beta' chains	100	250	363
481	ر د	1244	1534	emb X64172 SARP 	S.aureus rpli, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	100	224	291
487	2	1388	1188	gb M83994	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete	86	72	201
489		1 2737	1370	gb U21221+	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	66	1368	1368
1 503	2	1135	653	gb M83994	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	108	483
511	ю — — -	1613	2242	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	323	630
511	4	3122	2700	gb S76213	lasp23=alkaline shock protein 23 (methicillin resistant) (Staphylococcus aureus, 912, Genomic, 1360 nt]	96	423	423
1 520	- 1	1 758	1297	emb X72014 SAFI	IS.aureus fib gene for fibrinogen-binding protein	1 66 1	540	540
520	ر د – ا	1436	1801	emb X72013 SAFI	IS.aureus fib gene for fibrinogen-binding protein	1 66 1	221	366
1 526	-	1 2150	1 1092	dbj D17366 STAA	D17366 STAA Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	1 66 1	641	1059

Table 1

S. aureus - Coding regions containing known sequences

Contig	IORF	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt
528	2	288	1 963	gb L19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	6	260	906
528	e 	1098	1 2870	gb L19300 	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	ი ი	866	1773
530	; 	e 	434	gb U31979 	Staphylococcus aureus chorismate synthase (arcc) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (arcb) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	66	432	432
230	2	1211	1 2395	gb U31979 	Staphylococcus aureus chorismate synthase (arcc) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (arcb) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	91	1185	1185
530	m 	2409	2801	gb U31979 	Staphylococcus aureus chorismate synthase (aroc) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	88	181	393
530	4	1 2690	3484	gb L05004 	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	75	195
530	S	3482	4792	gb L05004	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	66	905	1311
530	9	4790	5380	gb L05004	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	196	591
1 539		e	1 338	emb X76490 SAGL	IS.aureus (bb270) glnA and glnR genes	66	336	336
539	- 5	1 336	1 527	emb X76490 SAGL	(S.aureus (bb270) glnA and glnR genes	100	189	192
554		727	365	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8F, cap8B, cap8U, cap8U, cap8V, complete cds	100	5.4	363
554	5	2175	1252	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8F, cap8H, cap8L, cap8H, cap8N, cap8N, cap8P, cap8	66	918	924
554	ю 	1574	1374	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8F, cap8F, cap8H, cap8I, cap8V, cap8F, cap8P, complete cds	96	122	201
584	7 -	1019	1 705	gb U21221	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	66	306	315
1 587	_. –	1475	1 4288	emb Z18852 SACF	S.aureus gene for clumping factor	- 86	2588	2814
1 598		1 3881	1953	dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	- 66	1873	1929

Table 1

S. aureus - Coding regions containing known sequences

11 ·	Contig ORF S ID ID (Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
605		2	745	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	86	338	744
1 609 1		1628	816	emb X76490 SAGL	S.aureus (bb270) glnA and glnR genes	100	495	813
614	1	1280	642	gb M32103	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	- 66	639	639
626	1 - 2	2508	1255	gb M63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	225	1254
626	2 - 3	3315	2284	gb M63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	66	838	1032
629	1	1999	1001	emb X17688 SAFE	1S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	66	066	666
629	2 - 1	1407	1195	emb X17688 SAFE	IS.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	86	194	213
631	2 5	5126	3228	emb 218852 SACF	S.aureus gene for clumping factor	82	489	1899
632		·	551	emb Z30588 SAST	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	66	549	549
632	2 - 5	529	1323	emb 230588 SAST	18.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	66	795	195
651		1909	1070	gb L19300 	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	1 66	478	840
657	2 1	1800	1105	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	456	969
662	1 9	806	456	emb X13404 SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	100	369	453
1 662 1	2 2	230	475	emb X13404 SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	100	246	246
662	3 7	746	1399	emb X13404 SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	- 66	653	654
1 682	1 9	926	480	gb M63177		100	136	477
685		1182	592	 db 10650001	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	86	534	591
685	2 - 1	1716	1153	db U65000	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	96	564	564
1 697	1	3	527	gb M63177	S.aureus sigma factor (plaC) gene, complete cds	100	195	525
1 697	2 4	485	784	gb M63177	S.aureus sigma factor (plaC) gene, complete cds	97	280	300

Table 1

S. aureus - Coding regions containing known sequences

+		+	+			+	+	
Contig	ORF	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
710		15	503	dbj D86240 D862 	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB,	66	217	489
1 733		26	1 205	gb M80252	Staphylococcus aureus norAl199 gene (which mediates active efflux of fluoroquinolones), complete cds	97	140	180
741		1736	1197	dbj D83951 STAL	Staphylococcus aureus DNA for LukM component, LukF-PV like component, complete cds	81	522	540
1 752		1 1	1 636	emb Y00356 SASP	Staphylococcus aureus V8 serine protease gene	1 66	618	636
1 752	2 -	588	926	emb Y00356 SASP	Staphylococcus aureus V8 serine protease gene	1 66	340	369
1 756	-	1308	1 709	emb X01645 SATO	Staphylococcus aureus (Wood 46) gene for alpha-toxin	86	567	009
777		1582	1 950	emb 249245 5A42	S.aureus partial sod gene for superoxide dismutase	1 66	429	633
1 780	П	1111	1 557	gb U20503	Staphylococcus aureus MHC class II analog gene, complete cds	96	550	555
1 784	7	7.3	1 687	19510635291	Staphylococcus aureus novel antigen gene, complete cds	66	568	615
197	1	182	544	dbj D14711 STAH	Staphylococcus aureus HSP10 and HSP60 genes	86	363	363
1 798	7	532	302	emb X58434 SAPD	1S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, I dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	95	196	231
823		۳ 	1 467	gb 877055 	recf cluster: dnaA=replisome assembly proteingyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	ი ი	156	465
848		348	175	gb L25288 	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	66	174	174
848	5	476	318	gb L25288 	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	100	131	159
998		792	397	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	66	395	396
883	1		1 285	dbj D90119 STAN	S. aureus norA gene	1 66	131	285
884	-	909 1	334	emb X52543 SAAG	IS.aureus agrA, agrB and hld genes	1 86	265	273
1 884	1 2	716	522	emb X52543 SAAG	IS.aureus agrA, agrB and hld genes	100	195	195
912	7	517	681	emb 230588 sAST	15.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	- 66	163	165
1 917		7	1 265	gb M64724	S.aureus tagatose 6-phosphate isomerase gene, complete cds	1 66	247	264
917	1 2	1 238	1 396	gb M64724	S. aureus tagatose 6-phosphate isomerase gene, complete cds	95	147	159
918		2426	1215	emb X93205 SAPT	emb X93205 SAPT S.aureus ptsH and ptsI genes	1 66	1212	1212
1		1	1		+	-		

Table 1

S. aureus - Coding regions containing known sequences

Contig ORF ID ID	IORF	Start (nt)	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt
1 967			411	dbj D90119 STAN	S. aureus norA gene	16	395	411
991		672	1 337	emb X52543 SAAG	lS.aureus agrA, agrB and hld genes	66	336	336
1000		1117	845	gb L14017 	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	78	190	273
1001		1 498	1 265	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	66	234	234
1010			1 285	gb U21221	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	66	224	285
1046		1 656	1 330	emb{X72700 SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	85	205	327
1060		480	1 286	emb X58434 SAPD	1S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	66	180	195
1073		1176	1 589	gb K02985	S.aureus (strain RN450) transposon In554 insertion site	100	131	588
1079		m 	1 230	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	66	228	228
1079	2	218	484	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	100	267	267
1079	რ — — -	1 460	645	dbj D86240 D862	<pre>IStaphylococcus aureus gene for unkown function and dlt operon dltA, dltB,</pre>	1000	186	186
1092		1 289	146	emb X58434 SAPD	1S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	86	124	144
1143			243	gb M63177	S.aureus sigma factor (plaC) gene, complete cds	66	243	243
1157		2	136	emb 248003 SADN S.aureus	S.aureus gene for DNA polymerase III	1 6 1	127	135
1189		1 720	361	gb S74031	norA=NorA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	66	360	360
1190		7	283	gb M21854 	S.aureus agr gene encoding an accessory gene regulator protein, complete cds	100	282	282
1190	7	1127	888	emb X52543 SAAG	IS.aureus agrA, agrB and hld genes	100	240	240
1225		- 2	163	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	97	124	1 162
1243		2	529	dbj D86240 D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	66	495	528
1244		1	1 210	gb 874031	norA=NorA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	100	210	210
1301	1	41	472	emb X76490 SAGL S.aureus	S.aureus (bb270) glnA and glnR genes	66 1	299	432
	 					++		1 - 1

Table

S. aureus - Coding regions containing known sequences

13 136	IORF -	Start (nt)	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt
Chi 1991 1992 1993 1994 1995 1	18	1	326	emb X64172 SARP	rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein hypothetical protein ORF202, DNA-directed RNA polymerase beta lains	86	277	308
675 409 1086240 108624 1086240 1086240 1086240 1086240 1086240 1086240 1086240 1086240 1086240 1086240 1086240 1086240 1086240 1086240 10864240 108	7	1	175	dbj D28879 STAP	aureus gene for penicillin-binding protein 1,	86	139	174
1324 991(0733741 Staphylococcus aureus type 8 capaule genes, cap80, cap80	1346	1	675		aureus gene for unkown function and dlt operon dltA, genes,complete cds	86	672	672
1922 dph 190336 Staphylococcus aureus alpha-hemolysin of methicillin resistance (femA) 100 180	644	1	324		aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8H, c	66	321	321
1811 emb X17688 SARE S. aureus factor essential for expression of methicillin resistance (femA) 100 180	-		192	1gb1M905361	aureus alpha-hemolysin gene, 3'	1 86	192	192
1402 dbj DB6E240 DB6E2 Staphylococcus aureus gene for unkown function and dit operon ditk, ditb, 100 402 4	8	:	181	 emb X17688 SAFE	factor essential for expression of methicillin resistance omplete cds, and trpA gene, 3' end	100	180	180
402 [db] 1086240 10862 Staphylococcus aureus game for unkown function and dit operon dita, ditb, 100 402 208 gb M53171 S.aureus signa factor [plac] game, complete cds 207 402 gb U66641 Staphylococcus aureus DNA fragment with class II promoter activity 99 131 400 gb L25426 Staphylococcus aureus pencillin-binding protein 2 [bbp2] game, complete 99 153 400 gb L25426 Staphylococcus aureus pencillin-binding protein 2 [bbp2] game, complete 99 153 400 gb L25426 Staphylococcus aureus games for ORF37; HSP20; HSP70; HSP40; ORF35, complete 100 358 400 gb L25426 Staphylococcus aureus games for ORF37; HSP20; HSP70; HSP40; ORF35, complete 100 358 400 1030690 STAN Staphylococcus aureus choicing lames, complete cds 400 400 464 [emb]X17679 SKCO Staphylococcus aureus choicing lames synthase (arcb) and classific diphosphate 88 178 464 [emb]X17679 SKCO Staphylococcus aureus games for Coagulase 1398 400 11784 400	7		346	1gb U605891	aureus novel antigen gene, complete	66	345	345
100 100	-		402	i ı	aureus gene for unkown function and dlt operon dltA, genes,complete cds	100	402	402
402 gb U66664 Staphylococcus aureus DNA fragment with class II promoter activity 99 131 156 emb X17688 SAFE S.aureus factor essential for expression of methicillin resistance (femA) 99 153 400 gb L25426 Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete 99 399 1398 gb U51132 Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 100 358 398 gb U51132 Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o- 97 272 328 gb U31132 Staphylococcus aureus o-succinylbenzoic acid GoA ligase (mene), and o- 97 272 464 emb X17679 SACO Staphylococcus aureus complete cds omplete cds omplete cds of hydroauinate synthase (arob) and Kinase (ndA) genes, complete cds omplete cds openes, partial cds 98 347 464 emb X17679 SACO Staphylococcus aureus coa gene for coagulase 1784 gb U311779 Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV30 165-238 87 82 1784 gb U311779 Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV30 165-238 87 64s 1884 gb U311779 Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 97 120 281 db U30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 97 120 281 db U30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 97 120 281 db U30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 97 120 281 db U30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 97 120 281 db U30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 97 120 281 db U30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 97 120 281 db U30690 STAN Staphylococcus aureus genes for ORF37; HSP40; ORF35, complete 98 178 281 db U30690 STAN Staphylococcus aureus genes for ORF3	4	. 4	1 208	gb M63177	sigma factor (plaC) gene, complete	66	207	207
156	-		1 402	gb U66664	aureus DNA fragment with class II promoter	1 66	131	402
400 qpi125426 Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete 99 399 399 399 399 cds dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 100 358 cds dbj D30690 STAN Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o- 97 272 succinylbenzoic acid synthetase (menc) genes, complete cds succinylbenzoic acid synthetase (menc) and nucleoside diphosphate 98 250 kinase (ndk) genes, complete cds, dehydroauinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds 464 emb X17679 SACO Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV30 165-235 87 82 RNA spacer region 1784 gb U11779 Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 88 178 cds dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 97 120	8		156		essential for expression of methicillin resistance cds, and trpA gene, 3' end	66	153	153
398 dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP40; ORF35, complete 100 358 100	7		400	gb L25426	aureus penicillin-binding protein 2 (pbp2) gene,	66	399	399
398 gb U51132 Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-	77	ω	398		genes for ORF37; HSP20; HSP70; HSP40; ORF35,	100	358	381
328 gb U31979 Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate 98 250	6		398	gb U51132 	aureus o-succinylbenzoic acid CoA ligase (mene), and ic acid synthetase (menc) genes, complete cds	97	272	396
464 mmb KX7679 SACO Staphylococcus aureus coa gene for coagulase 98 347 1784 gb U11779 Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV30 16S-23S 87 82 1784 1784 gb U11779 Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 88 178 178 128 dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 97 120	61	ω,	328	gb U31979 	chorismate synthase (aroc) and nucleoside complete cds, dehydroauinate synthase (arof nosphate synthetase homolog (gerCC) genes,	86	250	291
1784 gb U11779 Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV30 16S-23S 87 82 RRNA spacer region rRNA spacer region 128 128 120 281 dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 97 120 281 dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 97 120	83	2	464	mb X17679 SACO		86	347	369
238 dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 88 178	21	0.7	1784	gb U11779	methicillin-resistant ATCC 33952	87	82	387
281 dbj D30690 STAN Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete 97 120 cost cds	47		1 238	dbj D30690 STAN	genes for ORF37; HSP20; HSP70; HSP40; ORF35,	88	178	237
	45:		281	dbj D30690 STAN	genes for ORF37; HSP20; HSP10; HSP40; ORF35,	1 16	120	171

Table

S. aureus - Coding regions containing known sequences

		÷				+		
Contig	ž ::	Start (nt)	stop (nt)	match acession	marcn gene name	jercent ident	length	length
3011	. - .	1 793	1 398	emb X62992 SAFN	IS.aureus fnbB gene for fibronectin binding protein B	93	72	396
3019		2 	1 235	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	97	234	234
1 3023	-	81	1 233	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	87	100	153
3029	 	06	287	gb U51133 jb U51133	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	100	135	198
3039		18	164	gb U51133	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	97	135	147
3039	7	1 70	327	gb U51133 	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	77	183	258
3056		e 	215	emb X64172 SARP	S.aureus rpll, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	66	213	213
3059		- - - -	261	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP10; HSP40; ORF35, complete cds	86	234	261
3073	-	1 27	1 284	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	66	229	258
3074		2	397	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	96	250	396
3088		т — .	1 239	dbj D86727 D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	95	215	237
1 3097	 	1 444	1 244	emb 248003 SADN	S.aureus gene for DNA polymerase III	97	160	201
3102		1 307	155	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	97	142	153
3121	 	1 568	398	emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	100	88	171
3125		1 463	1 233	emb x89233 SARP	S.aureus DNA for rpoC gene	86	192	231
3133		2	175	emb 218852 SACF	S.aureus gene for clumping factor	96	154	174
3160	1	1 420	211	D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	1 68 1	197	210
3176		·	378	emb X58434 SAPD	IS.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	96	91	378
3192		1 420	211	gb J03479 	S.aureus enzyme III-lac (lacf), enzyme II-lac (lacf), and phospho-beta- galactosidase (lacG) genes, complete cds	86	72	210
3210	1 - 1	e -	1 143	gb M76714	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	96	141	141
		+					 	

Table 1

S. aureus - Coding regions containing known sequences

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Contig	ORF	Start	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt length
3232	m — —	2106	1282	gb L14017 	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	71	257	825
3538		2	394	emb X89233 SARP	S.aureus DNA for rpoC gene	- 66 -	350	393
3543		392	634	gb L11530}	Staphylococcus aureus transfer RNA sequence with two rRNAs	66 1	102	243
3555	. — -	637	320	emb 218852 SACF	S.aureus gene for clumping factor	66 1	307	318
3559		8	182	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	1000	141	180
3559	- 5	95	313	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	1 86	174	219
3563		278	141	gb U35773	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	100	61	138
3563	7	527	1 363	1gb1U357731	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (1gt) gene, complete cds	+	162	165
3566	- -	e	422	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	1 86 1	175	420
3588		7	262	gb L43098 	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	66	253	261
3593		8	1 350	gb J034794	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	66	345	348
3600		758	381	emb 218852 SACF	S.aureus gene for clumping factor	72	346	378
3602		788	396	emb 218852 SACF	S.aureus gene for clumping factor	86	319	393
3656	-	1013	528	emb 218852 SACF	S.aureus gene for clumping factor	84	403	486
3682		e 	236	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	100	231	234
3682		224	415	emb X64172 SARP 	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	112	192
3693	-	758	423	emb X62992 SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	229	336
3702		593	354	gb L11530	Staphylococcus aureus transfer RNA sequence with two rRNAs	96	81	240
3725	. –	924	463	emb 218852 SACF	S.aureus gene for clumping factor	71	367	462
3761		608	450	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	85	333	360
3767			402	emb X64172 SARP 	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	86	387	402
	-			-				

ORF nt length percent| HSP nt | length ident Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-|Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3emb|X64172|SARP |S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein | 17/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & (S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-(Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds emb|X64172|SARP |S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein | 17/112, hypothetical protein ORF202, DNA-directed RNA polymerase beta dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; |Staphylococcus aureus methicillin-resistance protein (mecR) gene and |Staphylococcus aureus peptidoglycan hydrolase gene, complete cds dbj|D10489|STAG |Staphylococcus aureus genes for DNA gyrase A and B, complete cds |dbj|D10489|STAG |Staphylococcus aureus genes for DNA gyrase A and B, complete cds dbj|D10489|STAG |Staphylococcus aureus genes for DNA gyrase A and B, complete cds |S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds |S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds |emb|X58434|SAPD |S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, emb|X58434|SAPD |S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, |emb|X16457|SAST |Staphylococcus aureus gene for staphylocoagulase emb|X17679|SACO |Staphylococcus aureus coa gene for coagulase | galactosidase (lacG) genes, complete cds |emb|Z18852|SACF |S.aureus gene for clumping factor |emb|X89233|SARP |S.aureus DNA for rpoC gene emb|X68425|SA23 |S.aureus gene for 23S rRNA unknown ORF, complete cds |emb|X89233|SARP |S.aureus DNA for rpoC gene ORF3, complete cds ORF3, complete cds match gene name | beta' chains beta' chains acession |gb|J04151| gb | U48826 | |gb|L14017| |gb|M767141 |gb|J03479| |gb|J04151| gb | L05004 | |gb|L05004| match (nt) 1 327 1 239 1 400 1 253 Contig |ORF | Start | ID |ID | (nt) | 1 793 11 1456 1 542 1 798 ლ — ო ო -1 --- _ _ -_ _ 3844 | 1

S. aureus - Coding regions containing known sequences

Table 1

S. aureus - Coding regions containing known sequences

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Contig	ORF	Start (nt)	Stop (nt)	match acession	l match gene name	percent	HSP nt length	ORF nt length
3910		ю	359	emb X58434 SAPD	18.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, I dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	66	278	357
3915			330	gb L14017 	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	175	330
3964	1	691	347	emb Z48003 SADN	18.aureus gene for DNA polymerase III	100	295	345
4007		199	390	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	1 86	163	192
4036	1	Е	371	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	1 66	339	369
4046	-	692	348	emb 218852 SACF	18.aureus gene for clumping factor	87	221	345
1 4060		П	375	emb 218852 SACF	S.aureus gene for clumping factor	96	271	375
4061		860	432	emb 248003 SADN	lS.aureus gene for DNA polymerase III	66	429	429
4062		909	304	gb L14017 	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	198	303
4085		58	402	gb U11786 	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV42 16S-23S FRNA spacer region	86	127	345
1 4088		2	301	gb L43098 	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	66	227	300
4093		5	772	emb X58434 SAPD	1S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	66	276	276
4097		1	402	emb 218852 SACF	S.aureus gene for clumping factor	74	307	402
4116		22	402	gb L05004 	Staphylococcus aureus dehydroquinate synthase (arob) gene, 3' end cds; 3- phosphoshikimate-1-carboxyvinyltransferase (arob) gene, complete cds; ORF3, complete cds	86	157	381
4125		240	401	gb U73374 	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F,	100	98	162
4149	1	35	247	gb J04151	S.aureus fibronectin-binding protein (fnbA) mRWA, complete cds	66	200	213
4151		629	366	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	87	150	264
4154		754	398	emb X64172 SARP 	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	66	297	357
4179			294	emb X64172 SARP 	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	86	240	294
	+		1 1 1 1 1 1 1			+		

Table 1

S. aureus - Coding regions containing known sequences

Contig	IORE	Start (nt)	Stop (nt)	match acession	match gene name	percent	HSP nt length	ORF nt
4203	-	-	1 255	emb X89233 SARP	S.aureus DWA for rpoC gene	1 66 1	239	255
1 4206			1 303	emb 218852 SACF	S.aureus gene for clumping factor	100	236	303
1 4206	- 5	195	344	emb 218852 SACF	S.aureus gene for clumping factor	95	65	150
4208	·	108	314	emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	68	9.2	207
4216		1 656	330	emb X58434 SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	86	326	327
1 4226	-	1 594	1 298	gb L11530	Staphylococcus aureus transfer RNA sequence with two rRNAs	1 6 1	132	297
4260		1 216	383	gb U11784	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV40 165-235 RRNA spacer region	83	141	168
1 4272		355	179	emb (248003 SADN	S.aureus gene for DNA polymerase III	100	164	177
1 4276	<u> </u>	4	177	emb X16457 SAST	emb X16457 SAST Staphylococcus aureus gene for staphylocoagulase	66	150	174
4277			270	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta chains	66	265	270
4282		691	1 377	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	86	282	315
4291		379	191	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	66	183	189
1 4295		e 	329	emb X16457 SAST	emb X16457 SAST Staphylococcus aureus gene for staphylocoagulase	94	144	327
4313		1 435	1 280	gb L11530	Staphylococcus aureus transfer RNA sequence with two rRNAs	100	94	156
4315		e 	185	gb J03479 	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	100	158	183
4315		101	1 310	gb J03479 	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	86	75	210
4327			1 294	gb L43098	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	86	294	294
1 4360		1 603	319	gb U02910	Staphylococcus aureus ATCC 25923 16S rRNA gene, partial sequence	100	116	1 285
4364		m 	146	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6	95	140	144
4388		167	310	emb X62992 SAFN	emb X62992 SAFN S.aureus fnbB gene for fibronectin binding protein B	73	119	144

Table 1

S. aureus - Coding regions containing known sequences

Contig	IORF IID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt
4401		2	313	emb X62992 SAFN	S.aureus fnbB gene for fibronectin binding protein B	1 6	243	312
4421	-	36	281	dbj D12572 STA2	Staphylococcus aureus rrnA gene for 23S ribosomal RNA	100	112	246
4426	. – -	e -	1 293	emb 218852 SACF	S.aureus gene for clumping factor	85	185	291
4428	i -	493	1 248	emb X64172 SARP 	S.aureus rpll, orf202, rpo8(rif) and rpoC genes for ribosomal protein 17/112, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	139	246
4462		~	271	emb X64172 SARP	S.aureus rpll, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	66	270	270
4466			1 240	emb 218852 SACF	S.aureus gene for clumping factor	1 66	231	240
4469	 		312	gb J03479	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	6	265	312
4485		m 	1 263	gb L43098 	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	1 86	259	261
4492		74	400	gb M86227	Staphylococcus aureus DNA gyrase B subunit (gyrB) RecF homologue (recF) and DNA gyrase A subunit (gyrA) gene, complete cds	85	104	327
4497		1 535	1 269	emb 218852 SACF	S.aureus gene for clumping factor	1 66	213	267
4529	-	2	172	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta 6 beta' chains	100	151	171
4547			1 300	emb X62992 SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	157	300
4554	1	318	160	emb 218852 SACF	S.aureus gene for clumping factor	84	126	159
4565		6	1 227	emb 218852 SACF	18.aureus gene for clumping factor	84	213	219
4569		67	1 222	emb 218852 SACF	S.aureus gene for clumping factor	1 86	127	144
4608		22	216	emb X58434 SAPD	IS.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	92	168	195
4614		1 464	234	emb 218852 SACF	S.aureus gene for clumping factor	86	169	231
4623	- 1	105	302	gb J04151	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	1 66	152	198
4632		18	1 206	gb J03479 	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta- galactosidase (lacG) genes, complete cds	86	183	189
4646	-		1 222	emb 218852 SACF	S.aureus gene for clumping factor	84	100	222
4687	- 1	1 2	166	gb J04151	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	1 86	156	165
								

S. aureus - Coding regions containing known sequences

percent HSP nt ORF nt ident length	75 155 156	98 103 153
match match gene name percent HSP nt ORF nt acession ident length length	L14017 Staphylococcus aureus methicillin-resistance protein (mecR) gene and 75 155 156 unknown ORF, complete cds	4703 1 1 153 emb X58434 SAPD S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, 98 103 153
match acession	gb L14017	emb X58434 SAPI
Stop (nt)	158	153
Contig ORF Start Stop ID (nt) (nt)	4695 1 313 158 gb	4703 1 1 153 emb
J IORF		4703 1 1
Contig	4695	4703